

SEQUENCE LISTING

<110> Skånemejerier AB

<120> NEW ENZYME AND ITS USE

<130> 75086

<150> US 60/320,139

<151> 2003-04-24

<150> US 60/481,598

<151> 2003-11-05

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 458

<212> PRT

<213> Unknown

<220>

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<400> 1

Met Arg Gly Pro Ala Val Leu Leu Thr Val Ala Leu Ala Thr Leu Leu
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Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
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Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
 35 40 45

Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
 50 55 60

Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
 65 70 75 80

Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
 85 90 95

Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
 100 105 110

Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
 115 120 125

Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly

130	135	140
Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu 145 150 155 160		
Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile 165 170 175		
Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr 180 185 190		
Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu 195 200 205		
Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly 210 215 220		
Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn 225 230 235 240		
Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala 245 250 255		
Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp 260 265 270		
Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro 275 280 285		
Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His 290 295 300		
Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His 305 310 315 320		
Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu 325 330 335		
Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu 340 345 350		
His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala 355 360 365		
Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser 370 375 380		

Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu
385 390 395 400

Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
405 410 415

Ser Ala Leu Pro Pro Asp Ala Leu Leu Val Ala Asp Gly Pro Cys Leu
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Pro Ser Leu Ser Gln Ala Lys Gly Cys Met Pro Leu Ser Pro Ala Ala
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Pro Thr Pro Ala Trp Leu Leu Trp Cys Trp
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120

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180

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240

tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacgggggtg
300

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360

gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg
420

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480

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720

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780

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840

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900

agaaggtgta cgatgccttc aaggacgccc accccaagct ccacgtctac aagaaggagg
960

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1020

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1080

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1200

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1260

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1320

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1380

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Lys Tyr

<210> 4

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<400> 4

Met Arg Gly Pro Ala Val Leu Leu Thr Val Ala Leu Ala Thr Leu Leu
 1 5 10 15

Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
 20 25 30

Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
 35 40 45

Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
 50 55 60

Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
 65 70 75 80

Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
 85 90 95

Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
 100 105 110

Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
 115 120 125

Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
 130 135 140

Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
 145 150 155 160

Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
 165 170 175

Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
 180 185 190

Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu
 195 200 205

Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly
 210 215 220

Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn
 225 230 235 240

Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala
 245 250 255

Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp
 260 265 270

Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro
 275 280 285

Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His
 290 295 300

Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His
 305 310 315 320

Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu
 325 330 335

Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu
 340 345 350

His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala
 355 360 365

Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser
 370 375 380

Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu

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720

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780

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840

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900

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960

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gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg
1080

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1140

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1200

tgctgggcat cgtgcccag gccaacgatg ggcacctagc tactctgctg cccatgctgc
1260

acacagaatc tgctcttccg cctgatggaa ggcctactct cctgccaag ggaagatctg
1320

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1380

tgtctgaggt cgcataacgc cccatggctc aaggaagccg ccgggagctg cccgcaggcc
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1740

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Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
20 25 30

Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
35 40 45

Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
50 55 60

Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
65 70 75 80

Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
85 90 95

Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
100 105 110

Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
115 120 125

Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
130 135 140

Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
145 150 155 160

Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile

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<212> PRT
<213> Unknown

<220>
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<212> PRT
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<220>
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Phe	Val	Thr	Met	Thr	Ser	Pro	Cys
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<212> PRT
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<210> 11
<211> 27
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<400> 11

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<210> 12

<211> 20

<212> DNA

<213> Unknown

<220>

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<400> 12

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<210> 13

<211> 18

<212> DNA

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<210> 14

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<210> 16
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<400> 16

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<210> 18
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